

| Table 1: Alpha Ia SNPs | | | | | | | | | | | |
|------------------------|---|-----------------------------------|--|---|----------------------|------------------|--------------------|--------------------|---------------------------------|----------------------|----------------------------|
| SNP Numbr (FINAL) | SNP location 'ont1, B=Ex Jar4, D=SpI E=SpVar2 | SNP Sequence (nucleotide context) | Nucleotide Change A=reference seq a=SNP sequence (A/a) | Repeats reference n= (range) n= (when applicable) | Type of nucleotide Δ | Location In Gene | Amino acid change? | Amino acid change? | Conservative amino acid change? | Type of2 amino subst | Δ Restriction Site? yes/no |
| 1 | A3465 | CAATCAGATTGT | G/T | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 2 | A3472 | TTTGTCAATTT | C/T | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 3 | A3501 | TATTTAAACAC | A/C | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | yes |
| 4 | A3719 | TACAAATGACT | A/G | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 5 | A3740 UD | AC repeat | (A/C)n | n=5-8 | insert/del | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 6 | A3754 UD | GC repeat | (G/C)n | n=6-12 | insert/del | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 7 | A3776 UD | AC repeat | (A/C)n | n=8-15 | insert/del | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| | A3727-78 | ... | (A/C)G/C(A/C)n | n=11 | insert/del | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 8 | A3828 | GAGGAAACATT | A/G | n=25 | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 9 | A3828 | TCAGCGAGAGC | C/A | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 10 | A4048 | TTTTTAAAAATG | A/T | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 11 | A4094 | GACATCAGTGGTGG | A/G | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 12 | A4109 | GGGTGAGTCAGC | A/G | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 13 | A4215 | GGTCGCGATCC | G/A | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | yes |
| 14 | A4315 | CCTCCCGCCGCGT | C/G | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 15 | A4385 | ATACCGGCCCT | G/A | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | yes |
| 16 | A4634 | CCTGCGGAGTC | C/T | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | yes |
| 17 | A4777 | CTGTGCGTTCG | G/A | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | yes |
| 18 | A4890 | GAAAGGCGTCATG | G/A | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 19 | A4893 | GGCGTCATGGAC | A/G | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 20 | A4858 | TGGCTCTCTAAGCC | T/C | | transversion | Exon1, 5' reg | no Δ aa | no Δ aa | | | yes |
| 21 | A4865 | GCCAGCTCTGGCT | C/T | | transition | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 22 | A5027 | GAGAATGAGCG | A/G | | insert/del | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 23 | A5291 | TTTTTTT | (T)n | n=7-9 | insert/del | Exon1, 5' reg | no Δ aa | no Δ aa | | | no Δ |
| 24 | A5862 | CTCAAAATGTA | A/G | | transition | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 25 | A5859 | GGAATTGCAT | T/C | | transition | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 26 | A5996 | TTTAATGGCCCTG | C/T | | transition | Exon1, 5'UTR | no Δ aa | no Δ aa | | | yes |
| 27 | A6158 | AGCCCGGGAGGTGG | G/C | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 28 | A6220 | CTCTCGGGAATG | G/C | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 29 | A6865 | CAGTCTCCCTGGT | T/G | | transition | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 30 | A6702 | GGCTGGAGGAGGCC | G/A | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 31 | A6804 | CCATCATCTCT | T/G | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | yes |
| 32 | A6944 | GGCAGCGGGATGGC | G/A | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 33 | A7141 | CCTCGCTCTCTG | G/T | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 34 | A7200 | TTTCAACACAGACA | A/C | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| 35 | A7273 | TCCAGTCTCTATT | T/C | | transversion | Exon1, 5'UTR | no Δ aa | no Δ aa | | | no Δ |
| Exon 2 / SpI Var 1 | | | | | | | | | | | |
| 36 | B267 | AGGAATGG | A/G | | transversion | Exon2, 5' intron | no Δ aa | no Δ aa | | | no Δ |
| 37 | B322 | CAAAATGTGA | T/C | | transversion | Exon2, 5' intron | no Δ aa | no Δ aa | | | yes |
| 38 | B504 | AATAGTATT | G/A | | transversion | Exon2, 5' intron | no Δ aa | no Δ aa | | | yes |
| 39 | B812 | TCTCCGAGA | C/T | | transversion | Exon2, 5' intron | no Δ aa | no Δ aa | | | yes |
| 40 | B776 | TCTCTCTCCATG | T/G | | transversion | Exon2, 5' intron | no Δ aa | no Δ aa | | | yes |
| 41 | B968 | AGGAAGTCT | | | | | | | | | |

none

| Reference Restriction Site (site/none) | SNP2 Restriction Site (site/none) | SNP location2 A=Exon1, B=Exon2 C=SpVar4, D=SpVar3 E=SpVar2 | (-) ALL n=280 (incl Correl) | (-12) ALL n=184 (no Correl) | (-13) BLACK n=43 (no Correl) | (-14) HISPANIC n=41 (no Correl) | (-15) CAU n (no Correl) |
|--|---|---|--------------------------------------|--------------------------------------|---------------------------------------|--|----------------------------------|
| Exon 1 | | | | | | | |
| none | none | A3465 | 0.388 | 0.400 | 0.410 | 0.421 | 0.378 |
| none | none | A3472 | 0.008 | 0.008 | 0.013 | 0.028 | 0.000 |
| none | none | A3501 | 0.008 | 0.014 | 0.084 | 0.000 | 0.000 |
| none | Maelll | A3719 | 0.005 | 0.003 | 0.013 | 0.000 | 0.000 |
| CfoI / MvrI / BssHl | CfoI / MvrI / BssHl | A3740 UD | | | | | |
| none | none | A3764 UD | | | | | |
| none | none | A3776 | | | | | |
| see above | see above | A3727-78 | | | | | |
| none | none | A3828 | 0.020 | 0.025 | 0.000 | 0.013 | 0.041 |
| none | none | A3928 | 0.008 | 0.009 | 0.031 | 0.000 | 0.008 |
| Drall / TruSI | Drall / TruSI | A4048 | 0.002 | 0.003 | 0.000 | 0.000 | 0.000 |
| none | none | A4084 | 0.002 | 0.003 | 0.013 | 0.000 | 0.000 |
| none | none | A4109 | 0.002 | 0.003 | 0.000 | 0.013 | 0.000 |
| HinfI | none | A4215 | 0.103 | 0.093 | 0.141 | 0.163 | 0.052 |
| none | none | A4315 | 0.058 | 0.058 | 0.083 | 0.038 | 0.051 |
| BstYI | MvrI / CfoI | A4385 | 0.185 | 0.140 | 0.138 | 0.054 | 0.178 |
| HinfI | none | A4634 | 0.057 | 0.048 | 0.000 | 0.163 | 0.021 |
| Maelll | Ddel / HinfI | A4777 | 0.130 | 0.118 | 0.285 | 0.175 | 0.051 |
| Acyl | none | A4890 | 0.002 | 0.003 | 0.000 | 0.000 | 0.005 |
| none | none | A4893 | 0.077 | 0.067 | 0.147 | 0.081 | 0.037 |
| none | none | A4956 | 0.012 | 0.015 | 0.078 | 0.000 | 0.000 |
| AluI / BglI | BglI | A4985 | 0.002 | 0.003 | 0.000 | 0.000 | 0.000 |
| none | none | A5027 | 0.102 | 0.080 | 0.216 | 0.088 | 0.030 |
| none | none | A5280 | | | | | |
| none | none | A5682 | 0.471 | 0.347 | 0.400 | 0.318 | 0.350 |
| none | none | A5859 | 0.009 | 0.003 | 0.012 | 0.000 | 0.000 |
| none | none | A5986 | 0.002 | 0.003 | 0.000 | 0.013 | 0.000 |
| none | none | A6158 | 0.004 | 0.005 | 0.028 | 0.000 | 0.000 |
| NciI/SacFI(2nd)/SmaI/MspI/Hpe | MspI/HpaII/ScrFI/NciI | A6220 | 0.002 | 0.003 | 0.000 | 0.000 | 0.005 |
| AvaI | BseAII/MroI/HpaII/MspI | A6685 | 0.007 | 0.005 | 0.000 | 0.013 | 0.005 |
| EcoRII | EcoRII | A6702 | 0.002 | 0.003 | 0.000 | 0.000 | 0.005 |
| Ilal | Ilal | A6804 | 0.005 | 0.005 | 0.000 | 0.000 | 0.010 |
| EcoRII/BstXI | EcoRII/BstXI | A6844 | 0.003 | 0.003 | 0.000 | 0.023 | 0.000 |
| none | none | A7141 | 0.055 | 0.043 | 0.000 | 0.138 | 0.043 |
| none | BpuAI | A7200 | 0.003 | 0.003 | 0.000 | 0.000 | 0.005 |
| none | none | A7273 | 0.003 | 0.003 | 0.000 | 0.000 | 0.008 |
| Exon 2 / Spl Var 1 | | | | | | | |
| none | none | B287 | 0.012 | 0.016 | 0.070 | 0.000 | 0.000 |
| none | HpyCHIV | B322 | 0.083 | 0.063 | 0.081 | 0.038 | 0.045 |
| none | SspI | B504 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 |
| PstI/Sfd/ HpyCHIV/BsmAI | PstI/Sfd/HpyCHIV/BsmAI | B612 | 0.463 | 0.482 | 0.287 | 0.525 | 0.565 |
| none | none | B776 | 0.002 | 0.003 | 0.012 | 0.000 | 0.000 |
| BstFI | BstFI | B888 | 0.030 | 0.021 | 0.023 | 0.025 | 0.020 |
| BamI / NlaIV | BamI / NlaIV | B1016 | 0.002 | 0.003 | 0.012 | 0.000 | 0.000 |
| Hpy188I | Ddel / Hpy188I | B1034 | 0.002 | 0.003 | 0.000 | 0.000 | 0.005 |
| Splice Variant 4 | | | | | | | |
| none | none | C563 | 0.068 | 0.028 | 0.060 | 0.071 | 0.010 |
| Splice Variant 3 | | | | | | | |
| none | none | D563 | 0.043 | 0.040 | 0.012 | 0.038 | 0.048 |
| none | TaqI | D578 | 0.006 | 0.006 | 0.028 | 0.000 | 0.000 |
| none | Ilal | D611 | 0.035 | 0.031 | 0.027 | 0.075 | 0.010 |
| Sau3AI/NdeII/BclI/DpnI | Ilal | D764 | 0.015 | 0.017 | 0.068 | 0.000 | 0.005 |
| none | none | D801 | 0.006 | 0.006 | 0.028 | 0.000 | 0.000 |
| Splice Variant 2 | | | | | | | |
| none | none | none | | | | | |

Schwinn ID# Table 2(A=exon1)

| Sequence | Range: | 1 | to | 7902 |
|------------|------------|-------------|------------|-------------|
| 10 | 20 | 30 | 40 | 50 |
| TAAACCATGT | TTTGGTATAA | ATGTAATAAT | AGAATGAGTT | CATGATATAA |
| ATTGGTGACA | AAACCATATT | TACATTATTA | TCTTACTCAA | GTACTATAAT |
| 110 | 120 | 130 | 140 | 150 |
| TTTTATATAA | TGTATACAAT | GTATAATATG | TGAAATATAT | ATGTATGCAT |
| AAATATATT | ACATATGTTA | CATATTATAC | ACTTTATATA | TACATACGTA |
| 210 | 220 | 230 | 240 | 250 |
| ATTTTCCCAT | GTATATAATT | AATACACATT | AACAAAAAAT | GAGAAAATAT |
| TAAAAAGGTA | CATATATTAA | TTAATGTAA | TTGTTTTTAA | CTCTTTTATA |
| 310 | 320 | 330 | 340 | 350 |
| TTTTATTTC | ATACATTCT | GTCTGACTTT | TCCAAATGTG | CTATTATGAG |
| AAAATAAAAG | TATGTAAAGA | CAGACTGAAA | AGGTTTACAC | GATAATACTC |
| 410 | 420 | 430 | 440 | 450 |
| AACAGCCCAT | CAGCAAGTGA | AGAGATGAGA | TAAAAATGTG | TCTGCACITG |
| TTGTCGGGTA | GTCGTTCACT | TCTCTACTCT | ATTTTACAC | AGACGTGAAC |
| 510 | 520 | 530 | 540 | 550 |
| GATATTGGG | GGGTGATTGA | ATATGCCCTCA | GCTTAGATTT | GCTATGCCGAG |
| CTATAAACCC | CCCAACTAAT | TATACGGAGT | CGAATCTAAA | CGATACGCTC |
| 610 | 620 | 630 | 640 | 650 |
| GACTTGACCT | CATATTCCIA | CCAATGATAGT | CCCACAGTGT | AGGGATGGGG |
| CTGAAGTGA | GTATAAGGAT | GGTACTATCA | GGGTGTCACA | TCCCTACCCC |
| 710 | 720 | 730 | 740 | 750 |
| ATTTGGAAA | ATGATGGCAA | AGACAGAATT | ACTATCTCAT | CAAAGACATC |
| TAAACCTTT | TACTACCGTT | TCTGTCTTAA | TGATAGAGTA | GTTTCTGTAG |
| 810 | 820 | 830 | 840 | 850 |
| AGAACACAAT | GCCTCTTTGG | AGAGCTGTGA | CTTGATACTG | CATCAATACC |
| TCTTGTGTTA | CGAAGAAACC | TCTCGACACT | GAACATGAC | GTAGTTATGG |
| 910 | 920 | 930 | 940 | 950 |
| TAGGAGAATT | AGTTGAAAAG | CCAAGTCTTT | GGGGTAGATA | CTAACATTAA |
| ATCCICTTAA | TCAACTTTTC | GGTTCAGAAA | CCCCATCTAT | GATTGTAATT |
| 1010 | 1020 | 1030 | 1040 | 1050 |
| TTCCATTGTG | TATTGTTTTC | TAAGGGAATG | ATAGACAGAT | TCCTTATTTT |
| AAGGTAACAC | ATAACAAAAG | ATTCCCTTAC | TATCTGTCTA | AGAAATAAAA |
| 1110 | 1120 | 1130 | 1140 | 1150 |
| GAAAGTCTCG | CCAATCAATG | CATGGGTTTA | TGTCCATTGC | TCAGCTCTTC |
| 1210 | 1220 | 1230 | 1240 | 1250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1310 | 1320 | 1330 | 1340 | 1350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1410 | 1420 | 1430 | 1440 | 1450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1510 | 1520 | 1530 | 1540 | 1550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1610 | 1620 | 1630 | 1640 | 1650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1710 | 1720 | 1730 | 1740 | 1750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1810 | 1820 | 1830 | 1840 | 1850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 1910 | 1920 | 1930 | 1940 | 1950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2010 | 2020 | 2030 | 2040 | 2050 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2110 | 2120 | 2130 | 2140 | 2150 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2210 | 2220 | 2230 | 2240 | 2250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2310 | 2320 | 2330 | 2340 | 2350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2410 | 2420 | 2430 | 2440 | 2450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2510 | 2520 | 2530 | 2540 | 2550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2610 | 2620 | 2630 | 2640 | 2650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2710 | 2720 | 2730 | 2740 | 2750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2810 | 2820 | 2830 | 2840 | 2850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 2910 | 2920 | 2930 | 2940 | 2950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3010 | 3020 | 3030 | 3040 | 3050 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3110 | 3120 | 3130 | 3140 | 3150 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3210 | 3220 | 3230 | 3240 | 3250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3310 | 3320 | 3330 | 3340 | 3350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3410 | 3420 | 3430 | 3440 | 3450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3510 | 3520 | 3530 | 3540 | 3550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3610 | 3620 | 3630 | 3640 | 3650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3710 | 3720 | 3730 | 3740 | 3750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3810 | 3820 | 3830 | 3840 | 3850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 3910 | 3920 | 3930 | 3940 | 3950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4010 | 4020 | 4030 | 4040 | 4050 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4110 | 4120 | 4130 | 4140 | 4150 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4210 | 4220 | 4230 | 4240 | 4250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4310 | 4320 | 4330 | 4340 | 4350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4410 | 4420 | 4430 | 4440 | 4450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4510 | 4520 | 4530 | 4540 | 4550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4610 | 4620 | 4630 | 4640 | 4650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4710 | 4720 | 4730 | 4740 | 4750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4810 | 4820 | 4830 | 4840 | 4850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 4910 | 4920 | 4930 | 4940 | 4950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5010 | 5020 | 5030 | 5040 | 5050 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5110 | 5120 | 5130 | 5140 | 5150 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5210 | 5220 | 5230 | 5240 | 5250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5310 | 5320 | 5330 | 5340 | 5350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5410 | 5420 | 5430 | 5440 | 5450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5510 | 5520 | 5530 | 5540 | 5550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5610 | 5620 | 5630 | 5640 | 5650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5710 | 5720 | 5730 | 5740 | 5750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5810 | 5820 | 5830 | 5840 | 5850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 5910 | 5920 | 5930 | 5940 | 5950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6010 | 6020 | 6030 | 6040 | 6050 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6110 | 6120 | 6130 | 6140 | 6150 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6210 | 6220 | 6230 | 6240 | 6250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6310 | 6320 | 6330 | 6340 | 6350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6410 | 6420 | 6430 | 6440 | 6450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6510 | 6520 | 6530 | 6540 | 6550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6610 | 6620 | 6630 | 6640 | 6650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6710 | 6720 | 6730 | 6740 | 6750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6810 | 6820 | 6830 | 6840 | 6850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 6910 | 6920 | 6930 | 6940 | 6950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7010 | 7020 | 7030 | 7040 | 7050 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7110 | 7120 | 7130 | 7140 | 7150 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7210 | 7220 | 7230 | 7240 | 7250 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7310 | 7320 | 7330 | 7340 | 7350 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7410 | 7420 | 7430 | 7440 | 7450 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7510 | 7520 | 7530 | 7540 | 7550 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7610 | 7620 | 7630 | 7640 | 7650 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7710 | 7720 | 7730 | 7740 | 7750 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7810 | 7820 | 7830 | 7840 | 7850 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |
| 7910 | 7920 | 7930 | 7940 | 7950 |
| TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT | TTTAAATGAT |

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|-------------|-------------|------------|------------|------------|-------------|------------|------------|-------------|-------------|
| CTTTCAGGAC | GGTTAGTTAC | GTACCCAAAT | ACAGGTAACG | AGTCGAGAAG | AGGTAGTCT | GAGTAAGGGG | GTCGTAGGGA | CTGTGTGGIG | AGATTTTAAUG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 | 1290 | 1300 |
| GGCTGCTGAT | GGTTCACCTT | CCTCACTTTT | GTCTACAAAT | CTCAATCCTG | CTGATTCCAC | AAATCCTACA | TCAAGCAATA | TCATTTTATG | AGTCTTTTCCA |
| CCGACGACTA | CCAAGTGGAA | GGAGTGAAAA | CAGATGTTA | GAGTTAGGAC | GACTAAGGTG | TTAGGATGT | AGTTCGTTAT | AGTAAAAATAC | TCAGAAAAGGT |
| 1310 | 1320 | 1330 | 1340 | 1350 | 1360 | 1370 | 1380 | 1390 | 1400 |
| CAACCACCCC | TTCAGGGGAT | TCTTCAATTT | CTGTACACCC | GGAAGTCTTC | AGAGTATCAC | CCTCAGAGCC | AGGCAAGAGG | GACCCCGGCT | AGGGTTTCAG |
| GTTGGTGGGG | AAGTCCCCTA | AGAAGTAAAA | GACAGTGTGG | CCTTCAGAAG | TCTCATAGTG | GGAGTCTCGG | TCCGTTCTCC | CTGGGGCCCGA | TCCAAAAGTC |
| 1410 | 1420 | 1430 | 1440 | 1450 | 1460 | 1470 | 1480 | 1490 | 1500 |
| GCTTTAGAGA | GTCCAGCTCT | GACTCCTTTT | GGCCATAGGA | CTAATGTGAT | ATGCCACCT | GGAGCCTGTG | CCCTCCTTTC | TAGACCATGC | CCTGGGACTC |
| CGAAATCTCT | CAGGTCGAGA | CTGAGGAAAA | CCGGTATCCT | GATTACACTA | TACGGGTGGA | CCTCGGACAC | GGGAGGAAAG | ATCTGGTACG | GGACCCTGAG |
| 1510 | 1520 | 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AGAATCCCTT | GCCCCAGATG | GCCACACAAT | CACITTCAGG | TCCATTCTCT | CTGGGCAGAC | AACATCACAA | ATGTGTGTAC | CCCAAGGCCT | GAGGCCAAGA |
| TCTTAGGGAA | CGGGGTCTAC | CGGTGTGTTA | GTGAAAGTCC | AGTAAGAGA | GACCCGCTCG | TTGTAGTGT | TACACACATG | GGGTCCCGGA | CTCCGGTTCT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 | 1690 | 1700 |
| AGGCAGCTTT | CTGGCTGTAG | GGGCTGAGGT | GTTCACACAC | ATTGTCATGG | CCCTCAAGA | CAAAGAACAA | GGGGGAAAGT | GAGAAGAAAA | GAAGCAGCCA |
| TCCGTCGAAA | GACCGACATC | CCCGACTCCA | CAAGTGTGTG | TAAACGTACC | GGGGAGTTCT | GTTCTTGT | CCCCCTTTCA | CTCTCTTTT | CTTCGTGCGT |
| 1710 | 1720 | 1730 | 1740 | 1750 | 1760 | 1770 | 1780 | 1790 | 1800 |
| GTGATCAGGG | CCAGCTCTTG | CAACTTAGCC | ATGTTGGGTC | ATTCTGATTA | AACCACTTAG | CTCAAGTGTA | GTGCTCAAGA | CACCTAGCAC | ATTCTCCAGC |
| CACTAGTCCC | GGTCGAGAAC | GTTGAATCGG | TACAACCCAG | TAAGACTAAT | TTGGTGAATC | GAGTTCACAT | CACGAGTTCT | GTGAATCGTG | TAAGAGGTGG |
| 1810 | 1820 | 1830 | 1840 | 1850 | 1860 | 1870 | 1880 | 1890 | 1900 |
| TGAATTTACC | AGTGTTTCATG | GACGACCTGG | GTTAGAAATA | TATTTGCGTA | TAAAGTAGCA | TACAAAATGA | GCAGAAAGGG | AGTTAATAAG | ATTAATAATA |
| ACTTAAATGG | TCACAAGTAC | CTGCTGGACC | CAATCTTTAT | ATAAAGCGAT | ATTTCATCGT | ATGTTTACT | CGTCTTTCCC | TCAATTATTC | TAATTATTAT |
| 1910 | 1920 | 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GAGTTAGTGA | ATATTATGAG | CTGAGTTTTT | GAGAAACGTA | ATTCTTTTCA | CAACACTAAT | AACAACCTTG | TGGGGGTTCA | TTGTCTCCCT | TTAAAAATTA |
| CTCAATCACT | TATAATACTC | GACTCAAAAA | CTCTTTGCAT | TAAAGAAAGT | GTTGTGATTA | TTGTTGGAAC | ACCCCCAAGT | AACAGAGGGA | AATTTTAAAT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 | 2090 | 2100 |
| GGAAACCAAG | GCITTGCCAT | GGTCGCATAG | GAGGGTCAGA | ATAGCATCTT | TATGACCCAG | AGCATACTCG | TCTCCACTCC | ACCTACCCAT | GTGTACAACT |
| CCTTTGGTTC | CGAAACGGTA | CCAGCGTATC | CTCCCAGTCT | TATCGTAGAA | ATACTGGGTC | TCGTATGAGC | AGAGGTGAGG | TGGATGGGTA | CACATGTTGA |
| 2110 | 2120 | 2130 | 2140 | 2150 | 2160 | 2170 | 2180 | 2190 | 2200 |
| CAGACACTTT | CTGGGATGTC | CACGTCAACT | ATTCTTTAAA | GAGTAACCAA | CAGATGGATA | GTTTCTGT | TGTGAATCAA | TGTAGGTGA | CTGAAAAATT |
| GTCTGTGAAA | GACCCCTACAG | GTGCAGTTGA | TAAGAAATTT | CTCATTTGGT | GTCTACCTAT | CAAAAGACAA | ACACTTAGTT | ACCATCCACT | GACTTTTTAA |
| 2210 | 2220 | 2230 | 2240 | 2250 | 2260 | 2270 | 2280 | 2290 | 2300 |
| GGTCTGAGA | GGTCGTTTGG | CAAGGATTGA | TGGTCACAGG | CTGAGAAGCA | GATTTGAAAG | ACCTACCTGC | TAGCAGCATA | AGAGCTGCTC | TTCCTTATCT |
| CCAAGACTCT | CCAGCAAAAC | GTTCTTAECT | ACCACTGTCC | GACTCTTCGT | CTAAACITTC | TGGATGGACG | ATCGTCGTAT | TCTCGACGAG | AAGGAATAGA |
| 2310 | 2320 | 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |
| TAGTATTAAC | TAGTTAATTA | TTGGAGGTGG | GTGCAGGGGT | GGATTATGTG | TATTCTTAAT | TGTTGTAGAG | TGGGAACTGG | GAGTTACAAA | GACTTTTGCA |
| ATCATAAATTG | ATCAATTAAT | AACCTCCACC | CACGTCGCCA | CCTAATACAC | ATAAGAAATTA | ACAACATCTC | ACCCTTGACC | CTCAATGTTT | CTGAAAAACGT |

| | | | | | | | | | |
|-------------|-------------|------------|-------------|------------|-------------|------------|-------------|-------------|--------------|
| 2410 | 2420 | 2430 | 2440 | 2450 | 2460 | 2470 | 2480 | 2490 | 2500 |
| AGTTTCGACC | TTGCAGAGCT | GAGCAATTTT | CAGTTGCTTT | GCTTGCTGAT | AGCACTGCCT | CCCTTATCTA | CCATGGAACA | CATCTTAATG | AAGAAATTTGC |
| TCAAAGCTGG | AACGTCTCGA | CTCGTTAAAA | GTCACGAA | CGAACGACTA | TCGTGACGAA | GGGAATAGAT | GGTACCTTGT | GTAGAATTAC | TTCTTAAACG |
| 2510 | 2520 | 2530 | 2540 | 2550 | 2560 | 2570 | 2580 | 2590 | 2600 |
| ATTACACAGCA | TCAGGTTAAT | GAATACAAAA | CAAAACAGTG | TATATCCCTC | TGATGGATGG | GATTCGGAA | GCACAGACAT | TATACACATA | TTTGATGATA |
| TAAGTGTCTGT | AGTCCAATTA | CTTATGTTTT | GTTTTGTAC | ATATAGGGAG | ACTACCTACC | CTAAGGCCTT | CGTGTCTGTA | ATATGTGTAT | AAACTACTAT |
| 2610 | 2620 | 2630 | 2640 | 2650 | 2660 | 2670 | 2680 | 2690 | 2700 |
| AAGTACTAGA | AGTGCAGGGA | ATTGAGGTCA | AGCTTCCTCC | TAAGGGGACT | GAATCCCAGA | GAGAGCAGGT | GACTTAGTAA | TGAGAAAGTGG | AGCTGTCTGT |
| TTCATGATCT | TCACGTCCCT | TAACTCCAGT | TCGAAGGAGG | ATTCCCCTGA | CTTAGGGTCT | CTCTCGTCCA | CTGAATCATT | ACTCTTCACC | TCGACAGACA |
| 2710 | 2720 | 2730 | 2740 | 2750 | 2760 | 2770 | 2780 | 2790 | 2800 |
| TCAAACCAGGA | TGCTCCTCCT | ATGGCAGGAA | ATTACAGTTTT | AAAAATATAT | TAAATTCAAA | TCAAATGTGT | TAGGTGTGAG | TTCTTATCCC | TACAGGTATG |
| AGTTGGTCCT | ACGAGGAGGA | TACCGTGCCT | TAAGTCAAAA | TTTTTATATA | ATTTAAGTTT | AGTTTACACA | ATCCACACTC | AAGAATAGGG | ATGTCCATAC |
| 2810 | 2820 | 2830 | 2840 | 2850 | 2860 | 2870 | 2880 | 2890 | 2900 |
| AGGCACAGGT | GGAGGACTTT | GTATACAATA | GAGAAATAAA | TACATATATT | AGGTCTTCCA | TGACATAGGA | TTTACTGACC | CTCTCATGGG | CATTCCTCTG |
| TCCGTCTCCA | CCTCCTGAAA | CATATGTTAT | CTCTTTATTT | ATGTATATAA | TCCAGAAGGT | ACTGTATCCT | AAATGACTGG | GAGAGTACCC | GTAAGGAGAC |
| 2910 | 2920 | 2930 | 2940 | 2950 | 2960 | 2970 | 2980 | 2990 | 3000 |
| AGGCATTTTG | AGATTATTG | CTATAAAGA | GCCTCCCAAA | CATTATCTCA | CTTAGAAAAG | GTAATCATAT | TAATATGATT | TGTTCCACAG | GAGAGAAATTT |
| TCCGTAAAC | TCTAAATAAC | GATATTTTCT | CGGAGGGTTT | GTAATAGAGT | GAATCTTTTC | CATTAGTATA | ATTATACTAA | AACAAGTGTC | CTCTCTTAAA |
| 3010 | 3020 | 3030 | 3040 | 3050 | 3060 | 3070 | 3080 | 3090 | 3100 |
| AAGTGCCACT | GCTTAAAGTT | ATCTCCTTGT | TCCTAGGTTT | AAGGAGACCT | AGTAAATAAG | AACATTCCAC | TTTGTTCTGCA | TCAATAAAGA | TGAAAGATGA |
| TTCACGGTGA | CGAATTTCAA | TAGAGGAACA | AGGATCCAAA | TTCCTCTGGA | TCATTTATTC | TTGTAAGGTG | AAACAGACGT | AGTTATTCT | ACTTTCTACT |
| 3110 | 3120 | 3130 | 3140 | 3150 | 3160 | 3170 | 3180 | 3190 | 3200 |
| CTTAGGAGGT | GGGAATTGGA | GTGGGAACA | TTTTTCTATG | TTCCCGATAT | TCTGAAACAC | ATGTGACTTT | ATTCAATCAC | AAGGTAAACA | GATTATGTAA |
| GAATCCTCCA | CCCTTAAACCT | CACCCTTTGT | AAAAAGATAC | AAGGGCTATA | AGACTTTGTG | TACACTGAAA | TAAGTTAGTG | TTCCATTTGT | CTAATACATT |
| 3210 | 3220 | 3230 | 3240 | 3250 | 3260 | 3270 | 3280 | 3290 | 3300 |
| TTTACCAGAA | AAAAAGTAAT | AAGACTGGTG | GTGCTAGGTT | TTCATACTCC | AGCTATTAAAT | GAATTAAGA | GAGTAACACT | CCTGAAAGGA | TACCATTTTC |
| AAATGGTCTT | TTTTTCATTA | TCTGACCCAC | CACGATCCAA | AAGTATGAGG | TCGATAATTA | CTTAATTTCT | CTCATTGTGA | GGACTTTCT | ATGGTAAAG |
| 3310 | 3320 | 3330 | 3340 | 3350 | 3360 | 3370 | 3380 | 3390 | 3400 |
| TCAAGAAAAAC | TGGAAGAAGAT | TGTGTGGCAT | TTAAAAATA | CCAAACTCTG | TGGCCATAAT | GCTCTTAAAA | TTCAATCTGTC | TAAAGAAAT | AGAAGTGAAT |
| AGTCTTTTG | ACCTTTTCTA | ACACACCGTA | AATTTTTAT | GGTTTGAGAC | ACCGGTATTA | CGAGAATTTT | AAGTAGACAG | ATTTCTTTAA | TCITTCACITTA |
| 3410 | 3420 | 3430 | 3440 | 3450 | 3460 | 3470 | 3480 | 3490 | 3500 |
| CATATTAAAT | AAGGTTTAGA | TATGTCCACT | TTATCTTCCT | GAAAAATATA | TTTCATTACA | ATCAGATTTG | TCATATTTTA | TCTGATTTTA | CTTGCTATTT |
| GTATAATTTA | TTCCAAATCT | ATACAGGTGA | AATAGAAGGA | CTTTTATATT | AAAGTAATGT | TAGTCTAAAC | AGTATAAAAT | AGACTAAAAAT | GAACGATAAA |
| 3510 | 3520 | 3530 | 3540 | 3550 | 3560 | 3570 | 3580 | 3590 | 3600 |
| AAACACACCTT | ATAATTTACT | TGCATATTTA | GAATTACAAT | ATTCTTAATA | TACTTCTTGA | TCTTAACAAA | ACCTAGGCCA | AATGTTAATC | AAATCAAGCT |
| TTTTGTGGAA | TATTAAATGA | ACGTATAAAT | CTTAATGTTA | TAAGAATTAT | ATGAAGAACT | AGAATTGTTT | TGGATCCGGT | TTACAATTAG | TTTAGTTCGA |

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|------------|-------------|-------------|------------|------------|------------|------------|------------|------------|-------------|
| 3610 | 3620 | 3630 | 3640 | 3650 | 3660 | 3670 | 3680 | 3690 | 3700 |
| GTTCAAAGTT | ACTTTATAGC | ACATTCTCTAT | GAACACACCA | TACACACAGC | AATATCTAGC | AAGGGTGTCA | ATTTTCGTT | ATTTTAAAA | GCTCATTTAA |
| CAAGTTTCAA | TGAAATATCG | TGTAAGGATA | CTTGTGTGGT | ATGTGTGCG | TTATAGATCG | TTCCACAGT | TAAAAAGCAA | TAAAAATTTT | CGAGTAAATT |
| 3710 | 3720 | 3730 | 3740 | 3750 | 3760 | 3770 | 3780 | 3790 | 3800 |
| AGAAGTTATT | TACTACAAAT | GACTCTACAC | ACACACACAC | GCGCGCGCGC | GCGCACACAC | ACACACACAC | ACACACAAAC | CTTTTAAAG | AAACGCTAGA |
| TCTTCAATAA | ATGATGTTTA | CTGAGATGTG | TGTGTGTGTG | GCGCGCGCGC | GCGGIGGTG | TGTGTGTG | TGTGTGTTG | GAAAAATTC | TTTGCATCT |
| 3810 | 3820 | 3830 | 3840 | 3850 | 3860 | 3870 | 3880 | 3890 | 3900 |
| ACCCAAACCC | CTCTAGGCCA | GAGGAAAACA | TTACAGCTGT | ATACGCACCT | GTGCCTGTTG | CCGTAGAGTA | ATACGGTAGC | AGCAGGAGAT | TACGGTACTA |
| TGGGTGGGG | GAGATCCGGT | CTCCTTTGT | AATGTCGACA | TATGCGTGAA | CACGGACAAC | GGCATCTCAT | TATGCCATCG | TCGTCTCTA | ATGCCATGAT |
| 3910 | 3920 | 3930 | 3940 | 3950 | 3960 | 3970 | 3980 | 3990 | 4000 |
| GCTGGGCTAC | TGCCTGAGTT | ACGTCAGCGA | GAGCTGCAAA | GTTCTTGTCT | ATTCTTTTCT | GGTGTGGGG | AGCTGAATAT | TAAAAGGGTG | ATTGTGGAGT |
| CGACCCGATG | ACGGACTCAA | TGCAGTCGCT | CTCGACGTTT | CAAGGAACGA | TAAGAAAAGA | CCACAGCCCC | TCGACTTATA | ATTTTCCCAC | TAACACCTCA |
| 4010 | 4020 | 4030 | 4040 | 4050 | 4060 | 4070 | 4080 | 4090 | 4100 |
| TACCGGTTAT | CTGCAATTTT | TTTTCTTTT | TTAATTTGAC | TCITTTTAAA | AAATGCAGGT | AAAGTGACAG | CGGTTACGGA | GCTTAAAGAC | ATCAGTGGTG |
| ATGGCCAATA | GACGTAAAAA | AAAAGAAAAG | AATAAAACTG | AGAAAAATTT | TTTACGTCCA | TTTCACTGTC | GCCAAGTCCT | CGAATTTCTG | TAGTACCCAC |
| 4110 | 4120 | 4130 | 4140 | 4150 | 4160 | 4170 | 4180 | 4190 | 4200 |
| GAGGGGTGAG | TCAGCGGGTG | CAAAAGGACA | AGGATTTGGT | GCCTCGGAGA | CACGGTCCCC | TCTCCGCCTC | CAGAGAAGAG | CAGGCAGGCA | GCTCCCCGGA |
| CTCCCCACTC | AGTCGCCCCAC | GTTTTCTGT | TCCTAAACCA | CGGAGCCTCT | GTGCCAGGGG | AGAGCGGGAG | GTCTCTTCTC | GTCCGTCCGT | CGAGGGCCCT |
| 4210 | 4220 | 4230 | 4240 | 4250 | 4260 | 4270 | 4280 | 4290 | 4300 |
| CCGAAGCCGG | GTCCGCATCC | CCCCGCGCGG | AGCTGGTGGC | TCAGCAGCGG | CGCTTCAGGT | GAGTGCGCCG | GGGCCGGCGT | CCCCCAGGGC | CGAGTGGGTG |
| GGCTTCGGCC | CAGGCGTAGG | GGGCGCGCGC | TGCACCACCG | AGTCGTCCGC | GCGAAGTCCA | CTCACGCGGC | CCCCGCCGCA | GGCGTCCCG | GCTCACCCAC |
| 4310 | 4320 | 4330 | 4340 | 4350 | 4360 | 4370 | 4380 | 4390 | 4400 |
| AGGGCAGACC | TCCCCCGCGG | TCTGTGTGAG | CGGAACCCCG | ACITTTCCCA | GCGCCTCCCG | CTTTTCCAC | CAGGTTTAT | ACCGCCCCCT | CTACCCCACC |
| TCCCGTCTGG | AGGGGCGGGC | AGACCACTCT | GCCTTGGGGG | TGAAAAGGGT | CGCGGAGGGC | GAAAAAGGTG | GTCCAAAATA | TGCCCGGGGA | GATGGGGTGG |
| 4410 | 4420 | 4430 | 4440 | 4450 | 4460 | 4470 | 4480 | 4490 | 4500 |
| CCCGATTCCC | TTACATCTTC | TGCGAAGTTG | CCTTCTACTG | AACAAGTGTG | TTTTTAACCC | TGTGTTTATC | ACCCTCGAGG | TAGGAGGAAA | AGGGTTTCTG |
| GGGCTAAGGG | AATGTAGAAG | ACGCTTCAAC | GGAAGATGAC | TTGTTACAG | AAAAATTGGG | ACACAAATAG | TGGGAGCTCC | ATCCTCCTT | TCCCAAAGAC |
| 4510 | 4520 | 4530 | 4540 | 4550 | 4560 | 4570 | 4580 | 4590 | 4600 |
| CAGTGGCAGC | TTTTTAATAC | CACCTGTGAG | GTCTCCAAC | TGCGATTTTA | ACAAGAGTCT | TTGCCCGAGG | TCCCACCTCA | GGGCCCCAAC | CCAGAAGGCA |
| GTCACCGTGC | AAAAATTATG | GTGGACACTC | CAGAGGTTGA | ACGCTAAAT | TGTTCTCAGA | AACGGGCTCC | AGGGTGGAGT | CCCGGGTTGG | GGTCTCCCGT |
| 4610 | 4620 | 4630 | 4640 | 4650 | 4660 | 4670 | 4680 | 4690 | 4700 |
| AGGTGGGCAC | TTCTCACGC | CGCGCTGTCC | TGCCGAGTCC | CTGCGGTAGG | TTCGCAGTTG | TGGAACCCCA | GGTTTCTTAC | GCAGATGGTG | GCCCCCAGCC |
| TCCACCCCGT | AAGGAGTGG | GCGCGACAGG | ACGGCTCAGG | GACGCCATCC | AAGCGTCAAC | ACCTTTGGGT | CCAAAAGATG | CGTCTACCAC | CGGGGGTCTGG |
| 4710 | 4720 | 4730 | 4740 | 4750 | 4760 | 4770 | 4780 | 4790 | 4800 |
| CAGAAAATCG | AAGCGGGCCC | CTGCCCGCTG | GCATGCCCGC | TTAATGTTTA | CGCCTGCAAA | ATCCGCAGTG | ACTGTGCTT | GCAAAGCTCC | CTCTGCAGAG |
| GTCITTTAGC | TTCCGCCGGG | GACGGCGGAC | CGTACGGCCG | AATTACAAAT | GCGGACGTTT | TAGCGTCCAC | TGACAGCGAA | CGTTTCGAGG | GAGACGCTC |
| 4810 | 4820 | 4830 | 4840 | 4850 | 4860 | 4870 | 4880 | 4890 | 4900 |

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|-------------|------------|-------------|------------|-------------|-------------|-------------|-------------|------------|-------------|
| GGACGTCCTC | CCCACCCCGT | CCCCGGCCAG | TCCCGCTACG | GCTGGCAGCT | GGAGCCCCCTC | GGGIGGCLAA | CAGTGAAGCT | IGGAAAGGCG | TCATGGACAG |
| CCTGCAGGAG | GGGTGGGCA | GGGGCGGTC | AGGGGATGC | CGACCGTCGA | CCTCGGGGAG | CCCACCGGT | GTCACCTCCGA | ACCTTCCGC | AGTACCTGTG |
| 4910 | 4920 | 4930 | 4940 | 4950 | 4960 | 4970 | 4980 | 4990 | 5000 |
| ACCTGGGTGG | CTTTCGTCT | TCGGGTCCCT | CCCCGGCTCG | CTCGGGACCT | GGCTCTCAAG | CCAGCTTGGC | TGGTGGACAG | ACCGGTGCGC | TCGTGCACAC |
| TGGACCCAGC | GAAAGACAGA | AGCCCAGGGA | GGGCCGAAGC | GAGCCCTGGA | CCGAGAGTTC | GGTCGAACCG | ACCACCTGTC | TGGCCACGCG | AGACGTGTGG |
| 5010 | 5020 | 5030 | 5040 | 5050 | 5060 | 5070 | 5080 | 5090 | 5100 |
| CGAGTGCAG | TTCCACCGGC | GTGAGATGA | GGCTGCTCGT | GGTCTGGCC | CTGAGGTCCC | TGGGTGCGAG | CTGTTCCCTC | TCCCAGGCGC | CCCCCTCCAG |
| GCTCACGCTT | AAGGTGGCCG | CACTCTTACT | CGCACGAGCA | CCAGGACCGG | GACTCCAGGG | ACCCAGCGTC | GACAAAGGAG | AGGGTCCGGC | GGGGGAGGTC |
| 5110 | 5120 | 5130 | 5140 | 5150 | 5160 | 5170 | 5180 | 5190 | 5200 |
| GTGACTGCGA | GGCAACCTGT | TCTAACGGAA | ACCGAGTACA | TCCTCCAGAA | TTCCCCGGCT | AGGATCCGTG | CGACACACTC | GCCAGCCGCA | GTGCCCCCTC |
| CACTGACGCT | CCGTTGGACA | AGATTGCCTT | TGGCTCATGT | AGGAGGTCTT | AAGGGGCCGA | TCCTAGGCAC | GCTGTGTGAG | CGGTGCGCGT | CAGCGGGGAG |
| 5210 | 5220 | 5230 | 5240 | 5250 | 5260 | 5270 | 5280 | 5290 | 5300 |
| CGGGGCTTCG | AGGATTTTAA | TTTCGTGGTA | CCTGCGCTCG | AAATCCAGAC | TTGAGCGCT | GGAGCCCTGGG | GTTTGGGGA | TTTGTTTTTT | TGTTTGTTTT |
| GCCCCGAAGC | TCCTAAAATT | AAAGCACCAT | GGACCGGAGC | TTTAGTCTG | AAGCTCGCGA | CCTCGGACCC | CAAAACCCCT | AAACAAAAAA | ACAAACAAAA |
| 5310 | 5320 | 5330 | 5340 | 5350 | 5360 | 5370 | 5380 | 5390 | 5400 |
| TCGCTTCGGA | TCCTGAATC | GGGCAGAGGT | GACTCAGTAG | AGTGGCTAG | GCAGGTTCCC | AGTGGTGGG | GCGCGAGATG | AGCTCCGAAG | TCGCTCCAC |
| AGCGAAGCCT | AGGACTTGAG | CCCGTCTCCA | CTGAGTCATC | TCACGGGATC | CGTCCAAGGG | TCACCACCCC | CGCGCTCTAC | TCGAGGCTTC | AGCGGAGGTC |
| 5410 | 5420 | 5430 | 5440 | 5450 | 5460 | 5470 | 5480 | 5490 | 5500 |
| CGCTGCCGGG | CGAAGCAGCT | TCTGGACCGC | AGAACCAACC | CGGCTCCCAA | CTGGTGTCCC | CCAACCCGTC | AAGCTCAGCA | CAGCCTCTTT | CCCTGGGGCG |
| GCGACGGCCC | GCTTCGTGCA | AGACCTGGCG | TCTTGTTGG | GCCGAGGGTT | GACCACAGGG | GTTGGGCGAG | TTGAGTCTGT | GTCGGAGAAA | GGGACCCCGC |
| 5510 | 5520 | 5530 | 5540 | 5550 | 5560 | 5570 | 5580 | 5590 | 5600 |
| CCTAGCTCAA | AGCCGCCCTT | CTCTTTGGC | TCCTTCAGGT | GGACGGGGTC | AAACGATGCC | CCGACGCCCTC | CTGGGTCTCA | GCACATATTC | CACACCTACG |
| GGATCGAGTT | TCGGCGGAAA | GAGAAACGCG | AGAAAGTCCA | CCTGCGGCCAG | TTTGCTACGG | GGCGTCGGAG | GACCCAGAGT | CGTGTATAAG | GTGTGGATGC |
| 5610 | 5620 | 5630 | 5640 | 5650 | 5660 | 5670 | 5680 | 5690 | 5700 |
| TCCCCTGACC | TGTGCTCCTA | GAACTGGGAG | AGAGCAGGAG | CCTTCGGTGG | GGCAGCTCAA | AATGTAGGTA | ACTGCGGGCC | AGGAGCAGCG | CCCAGATGCC |
| AGGGGACTGG | ACACGAGGAT | CTTCGACCTC | TCTCGTCCCT | GGAAGCCACC | CCGTCGAGTT | TTACATCCAT | TGACGCCCCG | TCCTCGTCGC | GGGTCTACGG |
| 5710 | 5720 | 5730 | 5740 | 5750 | 5760 | 5770 | 5780 | 5790 | 5800 |
| ATCGGTCCCT | GCCTTTGAGC | GTGACCGGCT | GATCTTTGG | TTTGAGGGAG | AGACTGGCGC | TGGAGTTTTG | AATCCGAAT | CATGTGCAGA | ATGCTGAATC |
| TAGCCAGGGA | CGGAAACTCG | CAGCTGCCGA | CTAGAAAACC | AAACTCCCTC | TCTGACCGCG | ACCTCAAAAC | TTAAGGCTTA | GTACACGTCT | TACGACTTAG |
| 5810 | 5820 | 5830 | 5840 | 5850 | 5860 | 5870 | 5880 | 5890 | 5900 |
| TTCCCCCAGC | CAGGACGAAT | AAGACAGCGC | GGAAAAGCAG | ATTCTCGTAA | TTCTGGAATT | GCATGTTGCA | AGGAGTCTCC | TGGATCTTCG | CACCCAGCTT |
| AAGGGGTGCG | GTCCTGCTTA | TTCTGTGCGG | CCTTTTCGTC | TAAGAGCATT | AAGACCTTAA | CGTACAACGT | TCCTCAGAGG | ACCTAGAAGC | GTGGGTGCGAA |
| 5910 | 5920 | 5930 | 5940 | 5950 | 5960 | 5970 | 5980 | 5990 | 6000 |
| CGGGTAGGGA | GGGAGTCCGG | GTCCCCGGGT | AGGCCAGCCC | GGCAGGTGGA | GAGGGTCCCC | GGCAGCCCCG | CGCGCCCCCTG | GCCATGCTT | TAATGCCCTG |
| GCCCCATCCCT | CCCTCAGGCC | CAGGGCCCCGA | TCCGGTCGGG | CCGTCCACCT | CTCCCAGGGG | CCGTGCGGGC | GCGCGGGGAC | CGGTACAGAA | ATTACGGGAC |
| 6010 | 6020 | 6030 | 6040 | 6050 | 6060 | 6070 | 6080 | 6090 | 6100 |
| CCCCCTCATG | TGGCCTTCTG | AGGGTTCCCA | GGGCTGGCCA | GGGTGTTTC | CCACCCGCGC | GCGCGCTCTC | ACCCCCAGCC | AAACCCACCT | GGCAGGGGCTC |

| | | | | | | | | | |
|------------|------------|------------|------------|-------------|-------------|------------|------------|------------|------------|
| GGGGAAGTAC | ACCGGAAGAC | TCCCAAGGGT | CCCGACCGGT | CCCAACAAAG | GGTGGGCGCG | CGCGCGAGAG | TGGGGGTGCG | TTTGGGTGGA | CCGTCCCGAG |
| 6110 | 6120 | 6130 | 6140 | 6150 | 6160 | 6170 | 6180 | 6190 | 6200 |
| CCTCCAGCCG | AGACCTTTTG | ATTCCCGGGT | CCCGCGCTCC | CGCCTCCGCG | CCAGCCCGGG | AGGTGGCCCT | GGACAGCCGG | ACCTCGCCCG | GCCCCGGCTG |
| GGAGGTCGGC | TCTGAAAC | TAAGGGCCGA | GGCGCGGAGG | GCGGAGGCGC | GGTCGGGCC | TCCACCGGA | CCTGTGGCC | TGGAGCGGGC | CGGGGCCGAC |
| 6210 | 6220 | 6230 | 6240 | 6250 | 6260 | 6270 | 6280 | 6290 | 6300 |
| GGACCATGGT | GTTTCTCTCG | GGAATGCTT | CCGACAGCTC | CAACTGCACC | CAACCGCCGG | CACCGGTGAA | CATTCCAAG | GCCATTCTGC | TCGGGGTGAT |
| CCTGGTACCA | CAAAGAGAGC | CCTTACGAA | GGCTGTCGAG | GTTGACGTGG | GTTGGCGGCC | GTGGCCACTT | GTAAGGTTT | CGGTAAGACG | AGCCCCACTA |
| 6310 | 6320 | 6330 | 6340 | 6350 | 6360 | 6370 | 6380 | 6390 | 6400 |
| CTTGGGGGGC | CTATTCTTT | TCGGGGTGCT | GGGTAACATC | CTAGTGATCC | TCTCCGTAGC | CTGTACCCGA | CACCTGCAC | CAGTCACGCA | CTACTACATC |
| GAACCCCCCG | GAGTAAGAAA | AGCCCCACGA | CCCATTTAG | GATCACTAGG | AGAGGCATCG | GACAGTGGCT | GTGGACGTGA | GTCAGTGGCT | GATGATGTAG |
| 6410 | 6420 | 6430 | 6440 | 6450 | 6460 | 6470 | 6480 | 6490 | 6500 |
| GTCAACCTGG | CGGTGGCCGA | CCTCCTGCTC | ACCTCCACGG | TGCTGCCCTT | CTCCGCCCATC | TTCAGGTCC | TAGGCTACTG | GGCCTTCGGC | AGGCTCTTCT |
| CAGTTGGACC | GCCACCGGCT | GGAGGACGAG | TGGAGGTGCC | ACGACGGGAA | GAGGCGGTAG | AAGCTCCAGG | ATCCGATGAC | CCGGAAGCCG | TCCAGAAGA |
| 6510 | 6520 | 6530 | 6540 | 6550 | 6560 | 6570 | 6580 | 6590 | 6600 |
| GCAACATCTG | GGCGGCAGTG | GATGTGCTGT | GCTGCACCGC | GTCCATCATG | GGCCTCTGCA | TCATCTCCAT | CGACCGCTAC | ATCGGCGTGA | GCTACCCGCT |
| CGTTGTAGAC | CCGCCGTCAC | CTACACGACA | CGACGTGGCG | CAGGTAGTAC | CCGAGACGCT | AGTAGAGGTA | GCTGGCGATG | TAGCCGCACT | CGATGGGCGA |
| 6610 | 6620 | 6630 | 6640 | 6650 | 6660 | 6670 | 6680 | 6690 | 6700 |
| GGCTACCCA | ACCATCGTCA | CCCAAGGAG | GGGTCTCATG | GCTCTGCTCT | GCGTCTGGGC | ACTCTCCCTG | GTCATATCCA | TTGGACCCCT | GTTCGGGTGG |
| CBCGATGGGT | TGGTAGCAGT | GGGTCTCCTC | CCCAGAGTAC | CGAGACGAGA | CGCAGACCCG | TGAGAGGGAC | CAGTATAGGT | AACCTGGGGA | CAAGCCGACC |
| 6710 | 6720 | 6730 | 6740 | 6750 | 6760 | 6770 | 6780 | 6790 | 6800 |
| AGGCAGCCCG | CCCCCGAGGA | CGAGACCATC | TGCCAGATCA | ACGAGGAGCC | GGGCTACGTG | CTCTTCTCAG | CGCTGGGCTC | CTTCTACCTG | CCTCTGGCCA |
| TCCGTCCGGC | GGGGGCTCCT | GCTCTGGTAG | ACGGTCTAGT | TGCTCCTCGG | CCCGATGCAC | GAGAAGAGTC | GCGACCCGAG | GAAGATGGAC | GGAGACCCGT |
| 6810 | 6820 | 6830 | 6840 | 6850 | 6860 | 6870 | 6880 | 6890 | 6900 |
| TCATCCTGGT | CATGTACTGC | CGCGTCTACG | TGGTGGCCAA | GAGGGAGAGC | CGGGGCTCTA | AGTCTGGCCT | CAAGACCGAC | AAGTCGGACT | CGGAGCAAGT |
| AGTAGGACCA | GTACATGACG | GCGCAGATGC | ACCACCGGTT | CTCCCTCTCG | GCCCCGGAGT | TCAGACCGGA | GTTCTGGCTG | TTCAGCCTGA | GCCTCGTTCA |
| 6910 | 6920 | 6930 | 6940 | 6950 | 6960 | 6970 | 6980 | 6990 | 7000 |
| GACGCTCCGC | ATCCATCGGA | AAACGCCCC | GGCAGGAGGC | AGCGGGATGG | CCAGCGCCAA | GACCAAGACG | CACTTCTCAG | TGAGGCTCCT | CAAGTTCTCC |
| CTCGAGGGCG | TAGGTAGCCT | TTTTGCGGG | CCGTCTCCG | TCGCCCTACC | GGTCGCGGTT | CTGGTTCTGC | GTGAAGAGTC | ACTCCGAGGA | GTTCAAGAGG |
| 7010 | 7020 | 7030 | 7040 | 7050 | 7060 | 7070 | 7080 | 7090 | 7100 |
| CGGGAGAAGA | AAGCGGCCAA | AACGCTGGGC | ATCGTGGTCG | GCTGCTTCGT | CCTCTGCTGG | CTGCCTTTTT | TCTTAGTCAT | GCCCCATTGT | AAGTCTTGAA |
| GCCCTCTTCT | TTCCGCCGTT | TTGCGACCCG | TAGCACCAGC | CGACGAAAGCA | GGAGACGACC | GACGGAAAAA | AGAATCAGTA | CGGGTAACCA | TTCAGAACTT |
| 7110 | 7120 | 7130 | 7140 | 7150 | 7160 | 7170 | 7180 | 7190 | 7200 |
| CACCCCTCAC | TTTAGCATCT | GGGGTCTTC | ACCCCTCTCG | GCTTCTGTTA | CCCCAGACTC | CCAGTCCCGG | ATGGAAGAGG | AAGGATTAGC | ATTTCAAAAC |
| GTGGGGAGTG | AAATCGTAGA | CCCCCAGAAG | TGGGAGGAGC | CGAAGACAAT | GGGGTCTGAG | GGTCAGGGCC | TACCTTCTCC | TTCTAATCG | TAAAGTTTGT |
| 7210 | 7220 | 7230 | 7240 | 7250 | 7260 | 7270 | 7280 | 7290 | 7300 |
| GCACAGCTCT | AGGGCAATTA | GAAAAGGCTC | CCTGTAGAA | AAGTGAATTT | TCATTCTCTT | TCTACTCCAG | TCTCATTTAT | ATTAGGCTCT | AGAGCACTTT |
| CGTGTCGAGA | TCCCGTTAAT | CTTTCCGAG | GGAACATCTT | TTCACTTAAA | AGTAAGAGAA | AGATGAGGTC | AGAGTAAATA | TAATCCAGGA | TCTCGTGAAA |

| | | | | | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|-------------|-------------|------------|------------|
| 7310 | 7320 | 7330 | 7340 | 7350 | 7360 | 7370 | 7380 | 7390 | 7400 |
| TTCGACTGTA | AAGTGGCTTC | CAACTGATGC | AGATTAATTG | GTCTCTTTAA | TAAGAATGTC | AACITTTTCTT | AATGCCCTATA | AGCACGGTGT | CAATTTAAAT |
| AAGCTGACAT | TTCACCGAAG | GTGACTACG | TCTAATTAAAC | CAGAGAAATT | ATTCTTACAG | TTGAAAAGAA | TTACGGATAT | TCGTGCACAA | GTTAATAATT |
| 7410 | 7420 | 7430 | 7440 | 7450 | 7460 | 7470 | 7480 | 7490 | 7500 |
| GCATCTGCTC | TCTCTAGTCT | CAGAGTCTCC | ACCAAGTGCT | TAGGCTGACT | GTGGAATGCC | ATTTTCACTC | TGCTACAGAA | TGCAAAATCT | CTTGGCCTGA |
| CGTAGACGAG | AGAGATCAGA | GTCTCAGAG | TGGTTCACGA | ATCCGACTGA | CACCTTACGG | TAAAAGTGAG | ACGATGTCTT | ACGTTTAAGA | GAACCGGACT |
| 7510 | 7520 | 7530 | 7540 | 7550 | 7560 | 7570 | 7580 | 7590 | 7600 |
| AAATAAGTAC | CATGCTTATT | CTGGACAAAT | GTGTGATTTT | ATTATTGCAT | TAGGTTATTC | ATAAGGGTTT | GTTATAATGG | TCTGTTTATG | TTCTATATCT |
| TTTATTTCATG | GTACGAATAA | GACCTGTTTA | CACACTAAAA | TAATAACGTA | ATCCAATAAG | TATTCCCAAA | CAATATTACC | AGACAAATAC | AAGATATAGA |
| 7610 | 7620 | 7630 | 7640 | 7650 | 7660 | 7670 | 7680 | 7690 | 7700 |
| GTGCTAANTT | TATTTTCTGG | ATTCAGTATG | GAAGGAATTA | TGGTCAGCCA | CTNAGAAAAA | AAAATGATTT | TATGTCCAAA | CCAATTTAAG | CCTTAAATAA |
| CACGATTNAA | ATAAAAGACC | TAAGTCATAC | CTTCCITTAAT | ACCAGTCGGT | GANTCTTTT | TTTTACTAAA | ATACAGGTTT | GGTTAAATTC | GGAATTTATT |
| 7710 | 7720 | 7730 | 7740 | 7750 | 7760 | 7770 | 7780 | 7790 | 7800 |
| TTAATCATAG | TATTTTCCAAT | AAGTAAATAC | TTATTTTTTT | ATTTTAATAA | TAAGTATTAA | AAACAAACAC | TTTCTCTTAT | CCAAAAATCA | TCCGGGAAAG |
| AATTAGTATC | ATAAAGGTTA | TTCAATTTATG | AATAAAAAAA | TAAAAATTAT | ATTCATAATT | TTTGTTTG | AAAGAGAATA | GGTTTTAGT | AGGCCCTTTC |
| 7810 | 7820 | 7830 | 7840 | 7850 | 7860 | 7870 | 7880 | 7890 | 7900 |
| TTACAAGATA | ACACTGTTTG | AAAATTATAC | AGTACNCATA | ATGTTACAAA | TCCAATTTTT | GCAAATGCTA | AATNGCGTT | TGTCAAAAT | AAATTGCTCA |
| AATGTTCTAT | TGTGACAAAC | TTTTAATATG | TCATGNGTAT | TACAATGTTT | AGGTTAAAAA | CGTTTACGAT | TTAANCGCAA | ACAGTTTTAA | TTTAACGAGT |

TC
AG

Schwinn IDF-Table 3 [B=ex n2]

Sequence Range: 1 to 1917

```

      10      20      30      40      50
ATAAACACTGAGGCTGTGTCTGTTGCATAAACTGCATCAGAGAATAAAA
TATTTGTGACTCCGACACAGACAACGTATTGTGACGTAGTCTCTTATTTT

      60      70      80      90     100
GGCATGTTTCAGATAACCGAATTTTAATATGGATTACTTGCATGGATTCCA
CCGTACAAGTCTATTGGCTTAAAATTATACCTAATGAACGTACCTAAGGT

      110     120     130     140     150
ACTTACTTTTCAATTTAGGCAAAACAATTTACATATGTGGACTCAGTCTG
TGAATGAAAAGTTAAATCCGTTTTGTAAATGTATACACCTGAGTCAGAC

      160     170     180     190     200
AGTTTTCACATTTTCATTTGGTAAAACTTCACAGCAGCTGTTGGTCACTGA
TCAAAGTGTAAGTAACCAATTTGAAGTGTCGTCGACAACCAAGTGACT

      210     220     230     240     250
GAGCCAGTGCAACCCTACCCACTGGGCCTGCTCCTGTAATTAATGACACA
CTCGGTCACGTTGGGATGGGTGACCCGGACGAGGACATTAATTACTGTGT

      260     270     280     290     300
CGCGGACCAAGTAGGAATGGTCTTTGAAGATATTGCAAAAGGGTGACA
GCGCCTGGTTTCATCCTTACCAGAACTTCTATAACGTTTTCCCACTGT

      310     320     330     340     350
GTCATAGGAGCTAGTCAGTCAAATGTGAGAACTCATATGTGTTTGGGAT
CAGTATCCTCGATCAGTCAGTTTACACTCTTTGAGTATACACAAACCCTA

      360     370     380     390     400
CATTTTAAACCGTTTAAAAATACAGAAAGATGTCTGTTTGATTGTTTTCT
GTAAATTTGGCAAATTTTATGTCTTTCTACAGACAACTAACAAAAGGA

      410     420     430     440     450
AGCCAATTGGCTTGCTGGCTTTCAAATAATATGTATAAATCTGTGTGTTT
TCGGTTAACCGAACGACCGAAAGTTTATTATACATATTTAGACACACAAA

      460     470     480     490     500
TCTTCCAGGGTCTTTCTTCCCTGATTTCAGCCCTCTGAAACAGTTTTTA
AGAAGGTCCCAGAAAGAAGGGACTAAAGTTCCGGGAGACTTTGTCAAAAAT
  G S F F P D F K P S E T V F>
  ____TRANSLATION OF DEB$HUM A1A-5'+EXON2+____>

      510     520     530     540     550
AAATAGTATTTTGGCTCGGATATCTAAACAGCTGCATCAACCCCATCATA
TTTATCATAAACCGAGCCTATAGATTGTGTCGACGTAGTTGGGGTAGTAT
  K I V F W L G Y L N S C I N P I I>
  ____TRANSLATION OF DEB$HUM A1A-5'+EXON2+SPLVAR1____>

      560     570     580     590     600
TACCCATGCTCCAGCCAAGAGTTCAAAAAGGCCTTTCAGAATGTCTTGAG
ATGGGTACGAGGTTCGGTTCTCAAGTTTTCCGGAAAGTCTTACAGAACTC
  Y P C S S Q E F K K A F Q N V L R>
  ____TRANSLATION OF DEB$HUM A1A-5'+EXON2+SPLVAR1____>

      610     620     630     640     650
AATCCAGTGTCTCCGAGAAAGCAGTCTTCCAAACATGCCCTGGGCTACA
TTAGGTCACAGAGGCGTCTTTCGTGAGAAGGTTTGTACGGGACCCGATGT
  I Q C L R R K Q S S K H A L G Y>
  ____TRANSLATION OF DEB$HUM A1A-5'+EXON2+SPLVAR1____>

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660 670 680 690 700
CCCTGCACCCGCCAGCCAGGCCGTGGAAGGGCAACACAAGGACATGGTG
GGGACGTGGGCGGGTCCGGCACCTTCCCGTTGTGTTCTGTACCAC
T L H P P S Q A V E G Q H K D M V>
___TRANSLATION OF DEB\$HUM A1A-5'+EXON2+SPLVAR1___>

710 720 730 740 750
CGCATCCCCGTGGGATCAAGAGAGACCTTCTACAGGATCTCCAAGACGGA
GCGTAGGGGCACCCTAGTTCTCTCTGGAAGATGTCCTAGAGGTTCTGCCT
R I P V G S R E T F Y R I S K T D>
___TRANSLATION OF DEB\$HUM A1A-5'+EXON2+SPLVAR1___>

760 770 780 790 800
TGGCGTTTGTGAATGGAAATTTTCTCTTCCATGCCCCGTGGATCTGCCA
ACCGCAAACACTTACCTTTAAAAAGAGAAGGTACGGGGCACCTAGACGGT
G V C E W K F F S S M P R G S A>
___TRANSLATION OF DEB\$HUM A1A-5'+EXON2+SPLVAR1___>

810 820 830 840 850
GGATTACAGTGTCCAAAGACCAATCCTCCTGTACCACAGCCCGGGTGAGA
CCTAATGTACACAGGTTTCTGGTTAGGAGGACATGGTGTGCGGGCCCACTCT
R I T V S K D Q S S C T T A R V R>
___TRANSLATION OF DEB\$HUM A1A-5'+EXON2+SPLVAR1___>

860 870 880 890 900
AGTAAAGCTTTTTGTCAGGTCTGCTGCTGTGTAGGGCCCTCAACCCCCAG
TCATTTTCGAAAAACGTCCAGACGACGACACATCCCGGGAGTTGGGGGTC
S K S F L Q V C C C V G P S T P S>
___TRANSLATION OF DEB\$HUM A1A-5'+EXON2+SPLVAR1___>

910 920 930 940 950
CCTTGACAAGAACCATCAAGTTCCAACCATTAAGGTCCACACCATCTCCC
GGAACGTCTTGGTAGTTCAAGGTTGGTAATTCCAGGTGTGGTAGAGGG
L D K N H Q V P T I K V H T I S>
___TRANSLATION OF DEB\$HUM A1A-5'+EXON2+SPLVAR1___>

960 970 980 990 1000
TCAGTGAGAACGGGGAGGAAGTCTAGGACAGGAAAGATGCAGAGGAAAGG
AGTCACTCTTGCCCCCTCCTTCAGATCCTGTCTTTCTACGTCTCCTTTCC
L S E N G E E V *>
___TRANSLATION OF DEB\$___>

1010 1020 1030 1040 1050
GGAATAATCTTAGGTACCCACCCCACTTCTCTCGGAAGGCCAGCTCTT
CCTTATTAGAAATCCATGGGTGGGGTGAAGGAAGAGCCTTCCGGTCGAGAA

1060 1070 1080 1090 1100
CTTGGAGGACAAGACAGGACCAATCAAAGAGGGGACCTGCTGGGAATGGG
GAACCTCCTGTTCTGTCTCTGGTTAGTTTCTCCCCCTGGACGACCCTTACCC

1110 1120 1130 1140 1150
GTGGGTGGTAGACCCAACTCATCAGGCAGCGGGTAGGGCACAGGGAAGAG
CACCACCATCTGGGTTGAGTAGTCCGTGCGCCCATCCCGTGTCCCTTCTC

1160 1170 1180 1190 1200
GGAGGGTGTCTCACAACCAACAGTTTCAAGATGATACGGAACAGCATTTT
CCTCCACAGAGTGTGGTTGGTCAAGTCTTACTATGCCTTGTCTGTAAG

1210 1220 1230 1240 1250
CCTGCAGCTAATGCTTTCTTGGTCACTCTGTGCCCCACTTCAACGAAAACC
GGACGTGATTACGAAAGAACCAGTGAGACACGGGTGAAGTTGCTTTTGG

1260 1270 1280 1290 1300
 ACCATGGGAAACAGAATTTTCATGCACAATCCAAAAGACTATAAATATAGG
 TGGTACCCTTTGTCTTAAAGTACGTGTTAGGTTTTCTGATATTTATATCC

1310 1320 1330 1340 1350
 ATTATGATTTTCATCATGAATATTTTGAGCACACACTCTAAGTTTGGAGCT
 TAATACTAAAGTAGTACTTATAAACTCGTGTGTGAGATTCAAACCTCGA

1360 1370 1380 1390 1400
 ATTTCTTGATGGAAGTGAGGGGATTTTATTTTCAGGCTGTTCACTTACTG
 TAAAGAACTACCTTCACCTCCCTAAAATAAAAGTCCGACAAGTGAATGAC

1410 1420 1430 1440 1450
 CACAGCCATTTCAACATGGCTTACAAAAGCCTTTCTTGACAAATCACTTA
 GTGTCGGTAAAGTTGTACCGAATGTTTTCGGAAAGAACTGTTTAGTGAAT

1460 1470 1480 1490 1500
 CCTGTTCCAGAACTCTGTTATGAGAATCCAGAGCTTATAATATTTTGNNNA
 GGACAAGGTCTTGAGACAATACTCTTAGGTCTCGAATATTATAAAACNNT

1510 1520 1530 1540 1550
 GGCAAAGATTGTCTCCCACTTACTTCTTATCTGCTTCACTATTGCATAAT
 CCGTTTTCTAACAGAGGGTAATGAAGAATAGACGAAGTGATAACGTATTA

1560 1570 1580 1590 1600
 GAATGAGCTTCACCTGTGGCATGTTGGAATGAGCCTTATGATCCAAGTAC
 CTTACTCGAAGTGGACACCGTACAACCTTACTCGGAATACTAGGTTTCATG

1610 1620 1630 1640 1650
 ATTATTTCCCGAACTTTGNAAAATACTAATGCTTAGCTTCAGACAATACTG
 TAATAAGGGCTTGAAACNTTTTATGATTACGAATCGAAGTCTGTTATGAC

1660 1670 1680 1690 1700
 ATGGNTCNCCAAAGNACTGTCTAACGCAGGAGTTTNCNAACATTTTTTGA
 TACCNAGNGGTTTCTNTGACAGATTGCGTCCTCAAANGNTTGTA AAAA ACT

1710 1720 1730 1740 1750
 TAGGAGGCCATTTGTTCTGGTAAAAGATCCAGTAGTCAACTCAACTTCAT
 ATCCTCCGGTAAACAAGACCATTTTCTAGGTCATCAGTTGAGTTGAAGTA

1760 1770 1780 1790 1800
 CTATTCCTACTTTTCTGCAAGAGCTTGGGGNACATGCTATATTTTGCTTT
 GATAAGGATGAAAAGACGTTCTCGAACCCNTGTACGATATAAAACGAAA

1810 1820 1830 1840 1850
 ATGTATACCNAATTTTGGTAAACCATAATAACTCAGTAAAAAAAAGTCG
 TACATATGGNTTAAAACCATTTGGTATTATTGAGTCATTTTTTTTTTCAGC

1860 1870 1880 1890 1900
 ACGCGGCCGCGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG
 TCGCGCCGGCGCTTAAGCTATAGTTCTGAATAGCTATGGCAGCTGGAGCTCC

1910
 GGGGGCCCCGGTACCCAA
 CCCCCGGGCCATGGGTT

Schwinn IDF-Table 4[C=Sp1v4]

Sequence Range: 1 to 1702

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      10      20      30      40      50
AAGACNAGTTGTGTTTTGGGTAAATNAAANANTCTCNTNNNGATTTTTTGN
TTCTGNTCAACACAAAAACCCATTTANTTTTNTNAGAGNANNNNCTAAAAACN

      60      70      80      90     100
TNAGGCCCTACAGTNTGCCAGGNATCTTCCAGGANTTTTGAACCCATTGC
ANTCCGGGATGTCTANACGGTCCNTAGAAAGGTCTNAAAACCTGGGGTAACG

     110     120     130     140     150
CTCTAAANTCNTTGGAAACTCTTGTACCCCTATTTTAACAGANAAAAAAT
GAGATTTNAGNAACCTTTGAGAACATGGGGATAAAATTGTCTNTTTTTTA

     160     170     180     190     200
CTGATCATTGTANGGAGNTTAAGGACTTGCCCAAGGCCAAGGGGACCCAT
GACTAGTAACATNCCTCNAATTCCTGAACGGGTTCGGGTTCCCCTGGGTA

     210     220     230     240     250
GATTTAAACCTGGTCTCCCTATTCTCAACNTGCACATTTTCCATAGCCCC
CTAAATTTGGACCAGAGGGATAAGAGTTGNACGTGTAAAAGGTATCGGGG

     260     270     280     290     300
CCCTTCCTCAAGAGAATGGGGGTAAACGTTTTCCCATTTGGATTAGGTGT
GGGAAGGAGTTCTCTTACCCCCATTTGCAAAGGGTAAACCTAATCCACA

     310     320     330     340     350
GCTGAGGATGCCAAGCCATATCCAAACTTTTTAATGTTCTGTTTCCTTGA
CGACTCCTACGGTTCGGTATAGGTTTGAAAAATTACAAGACAAAGGAACT

     360     370     380     390     400
GATTTGCCTCCAAATTAACCATGGCAAACATGCTGCCAAATCTCCAGCCC
CTAAACGGAGGTTTAATTGGTACCGTTTGTACGACGGTTTAGAGGTCGGG

     410     420     430     440     450
AGTCAAACCCAAGAGCAGGGCATCTGTGGAAGAATTTGGTGTCTGCACTT
TCAGTTTGGGTTCTCGTCCCGTAGACACCTTCTTAAACCAAGACGTGAA

     460     470     480     490     500
CTATCAGACTGCATCACATTTTTAGGAGTTAATGGCCTGGAATGTGATTA
GATAGTCTGACGTAGTGTA AAAATCCTCAATTACCGACCTTACACTAAT

     510     520     530     540     550
AGGCCTTGCAAGGAGGACATACTATGGCACGCTGGGGGAAGATGGGCATA
TCCGGAACGTTCTCTCTGTATGATACCGTGCGACCCCTTCTACCCGTAT

     560     570     580     590     600
GAAGAGTATGCAGAAGGGGCCACATTGGCCAAGAACAGTAAAATGCAGTT
CTTCTCATACGTCTTCCCCGGTGTAACCGGTTCTTGTCATTTTACGTCAA

     610     620     630     640     650
GCTGACAGGACACATATCGGGTGTTGTATTGAAGTTATTGATGACCAACC
CGACTGTCCTGTGTATAGCCCAACATAACTTCAATAACTACTGGTTGG

     660     670     680     690     700
ACAGTTCATAGAAACACTTTTGGGAAGTACATCCCTTTTAAAAATAAATG
TGTCAGTATCTTTGTGAAAACCTTCATGTAGGGAAAATTTTATTTTAC

     710     720     730     740     750
AAAGCAAATACGGCATAACTCACTCTCACTCACCTGTATTCCAACTTTTT
TTTCGTTTATGCCGTATTGAGTGAGAGTGAGTGACATAAGGTTGAAAAA
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760 770 780 790 800
 TTTTGTGGACAGAGGGGAATGGATTGTAGATATTTACCAAGAATTGC
 AAAACAAACCTGTCTCCCCTTACCTAACATCTATAAAGTGGTTCTTAACG
 R G M D C R Y F T K N C>
 _____TRANSLATION OF DEB\$HUM A1A-5'____>

810 820 830 840 850
 AGAGAGCATATCAAGCATGTGAATTTTATGATGCCACCGTGGAGAAAGGG
 TCTCTCGTATAGTTTCGTACACTTAAAATACTACGGTGGCACCTCTTTCCC
 R E H I K H V N F M M P P W R K G>
 _____TRANSLATION OF DEB\$HUM A1A-5'+SPLICE VAR4+.____>

860 870 880 890 900
 TTCAGAATGCTGATCTCCAGGTAGCTGGAGACCTAGGCAGTCTGCAAATG
 AAGTCTTACGACTAGAGGTCCATCGACCTCTGGATCCGTCAGACGTTTAC
 S E C *>
 _____>

910 920 930 940 950
 AGGAGTCAGCTGGAAGCTATGGCTATGTATTATGTGACATCGCTTGTTC
 TCCTCAGTCGACCTTCGATACCGATACATAATACTGTAGCGAACAAGG

960 970 980 990 1000
 TAATTTCTTTTACACAAGTGAAAACCTGGATATCCCAACCTTCTGGCCCA
 ATTAAGAAAAGTGTGTTCACTTTTGACCTATAGGGTTGGAAGACCGGGT

1010 1020 1030 1040 1050
 GTAGGTTTCATGGTTAAGACCTGGTAGTGAGAACATTTTAGGAACTATTT
 CATCCAAAGTACCAATTCTGGACCATCACTCTTGTAATCCTTGATAAA

1060 1070 1080 1090 1100
 GCTTGGGCAGGTAATTTTTCACTCTGATCAGCTACTTAATCAGAGCTT
 CGAACCCGTCATTAAAAAGTGAGACTAGTGTGATGAATTAGTCTCGAA

1110 1120 1130 1140 1150
 GACAACTTTCTCAATTGCTTCTGGGGCTGGTCTGCTCAGGTCCTTTGGC
 CTGTTTGAAAGAGTTAACGAAGACCCCGACCAGACGAGTCCAGGAAACCG

1160 1170 1180 1190 1200
 CAAAAAGATGCTGCCTCTGTGTGTGAATACTTGTGACTTAATTAAAGA
 GTTTTTTCTACGACGGAGACACACTTATGAACAACTGAATTAATTTCT

1210 1220 1230 1240 1250
 AAGAGCTCTGCTCATTAGCAAAGGGCACTGNNGCAGATGGGAGGTAAACT
 TTCTCGAGACGAGTAATCGTTTCCCGTGACNNCGTCTACCCTCCATTTGA

1260 1270 1280 1290 1300
 CTCCAGGGAAAAACCAAGTGAAAAGAAAGCAGAGGAGGCAAAATATGGAGA
 GAGGTCCCTTTTTGGTTCACTTTTCTTTCGTCTCCTCCGTTTATACCTCT

1310 1320 1330 1340 1350
 CATCAGAGGTATGCCTACCAGTTACTCTGATTTTTTTTACACTACTAGGAC
 GTAGTCTCCATACGGATGGTCAATGAGACTAAAAAATGTGATGATCCTG

1360 1370 1380 1390 1400
 TTTTAACTATGAAACCACTGCGCACAGCTCCAGTGGAGCCCAGTTGGAA
 AAAATTGATACTTTGGTGGACGCGTGTGAGGTCACCTCGGGTCAACCTT

1410 1420 1430 1440 1450
 CACTGTTTGCACCTGCCCCGTATCTGCAGACTGTCTGGGGAGCTGGGCT
 GTGACAAACGTGGACGGGGCATAGACGTCTGACAGGACCCCTCGACCCGA

1460 1470 1480 1490 1500
GAGCCAGGCTGCTGTGGTGCCATCCATCTTCAGAAAGCAATGGCAGCTGT
CTCGGTCCGACGACACCACGGTAGGTAGAAAGTCTTTCGTTACCGTCGACA

1510 1520 1530 1540 1550
GGCCCTCCTGGCCTCCANAACCCCTGGGGAGCAAGNATGAGTGGGAGATN
CCGGGAGGACCGGAGGTNTTGGGGACCCCTCGTTCNTACTCACCCCTCTAN

1560 1570 1580 1590 1600
ATCACTGGTGGGGGCTNAGGCTGACNAAAAGCAAGTTTAGGAATTTCAAT
TAGTGACCACCCCGANTCCGACTGNTTTTCGTTCAAATCCTTAAAGTTA

1610 1620 1630 1640 1650
NGGGGGGGACAACAAGCCCTNGCNCCCATCNAGCAATTAGGTCAATTCAC
NCCCCCCTGTTGTTTCGGGANCGNGGGTAGNTCGTTAATCCAGTTAAGTG

1660 1670 1680 1690 1700
GCCNCCCCAAGACCCAAATNTGGGNGGAGGGGGTTNNAGANTTTGGCCCT
CGGNGGGGTTCTGGGTTTANACCCNCCTCCCCCAANNTCTNAAACCGGGA

TC
AG

Schwinn IDF-Table 5 [D=Sp1V3]

Sequence Range: 1 to 1214

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      10      20      30      40      50
CCCTCATTGCNAACANTTGAAGCATNTTNAAGNGTGGCNTNCTTTTGT
GGGAGTAACGNTTGTNAACTTCGTANAANTTCCNCACCGNANGAAAAACA

      60      70      80      90     100
AACCAAAACCTGATTGGAAGCAGAAGTTGGGGGGGGGGGAAATTGGAAG
TTGGTTTTGGACTAACCTTCGTCTTCAACCCCCCCCCCCTTTAACCTTC

     110     120     130     140     150
CAAAAGGGACCGAACTTGAAGCNTGTACTNCCCAGACTTCTCATTGGAAG
GTTTTCCCTGGCTTGAACCTTCGNACATGANGGGTCTGAAGAGTAACCTTC

     160     170     180     190     200
CTCCAGGTCACAATCTTAGTNCTAATTTCAAGGTTCTGCCCAGTCGAGTC
GAGGTCAGTGTTAGAATCANGATTAAAGTCCAAGGACGGGTCAGCTCAG

     210     220     230     240     250
TAGACATTNCTGGGGCACCCCTTTAAGTGGTCTCCAGCACCCCTTCTAGGCA
ATCTGTAANGACCCCGTGGGAAATTCACCAGAGGTCGTGGGAAGATCCGT

     260     270     280     290     300
GGTGGCTTACAGGGAAGTCCACACTGCAAGCTCAGCTCACCACGACTCA
CCACCGAAGTGTCCTTCAGGTGTGACGTTTCGAGTCGAGTGGTGCTGAGT

     310     320     330     340     350
GGCTGACGGGGTAGTCAGCCATGCTCGGAGGCTGAATTTGGCAGGGACTT
CCGACTGCCCCATCAGTCGGTACGAGCCTCCGACTTAAACCGTCCCTGAA

     360     370     380     390     400
GCTGCCATCTCCCTGCCAAATGGTCTCTCGTGACTCAGAATCTCAAACCT
CGACGGTAGAGGGACGGTTTACCAGAGAGCACTGAGTCTTAGAGTTTGAA

     410     420     430     440     450
GTTTTAAAGAGAGGAAAAAAGTCACTTTTCGGGGATGAGGTTCTTGCCCA
CAAAATTTCTCTCCTTTTTTTCAGTGAAAGCCCTACTCCAAGAACCGGGT

     460     470     480     490     500
ACTCTGCTTTATATAAACACAGTCTATGGCTATTTTCAGTCTTCTGGATTT
TGAGACGAAATATATTTGTGTCAGATACCGATAAAGTCAGAAGACCTAAA

     510     520     530     540     550
TGAGAAGCAGCTGCAAGGATGAACGGATTGGTGTGGCCCAAATTAAAAA
ACTCTTCGTGACGTTCTTACTTGCCTAACCAACCGGGTTTAATTTTT

     560     570     580     590     600
GAAGAGTATTCAGTTCTTTTCAGTGTTTGGAGAAAGAAGACCAAAAGCATC
CTTCTCATAAGTCAAGAAAGTCACAAACCTCTTTCTTCTGGTTTTTCGTAG

     610     620     630     640     650
ATCTCACAGGGAGCAGAATGTGACCAGCCTGGCTAATGAGGAAATGAGAG
TAGAGTGTCCCTCGTCTTACACTGGTGGACCGATTACTCCTTTACTCTC

     660     670     680     690     700
GGATCCTCAACTTGAGAACCCGCTCTACTGAAGTCTGAACTTGAAAAAT
```

CCTAGGAGTTGAACTCTTGGGCGAGATGACTTCAGACTTGAACCTTTT

710 720 730 740 750
GGACACATTGGGTTTGGAGTAAGAATTCTTACTCTACAAAAGGATAAAAT
CCTGTGTAACCCAAACCTCATTCTTAAGAATGAGATGTTTTCTATTTTA

760 770 780 790 800
TGTGATCACATTGATGCATGATGCCTAGGATATTAAAAATGCATGATTAA
ACACTAGTGTAACCTACGTACTACGGATCCTATAATTTTACGTACTAATT

810 820 830 840 850
TTAAATGTTAGTCTACCTTGTGTTTTAAAGGGACACACACCCATGACATG
AATTTACAATCAGATGGAACACAAAATTTCCCTGTGTGTGGGTACTGTAC

G H T P M T>
____TRANSLATION____>

860 870 880 890 900
AAGCCAGCTTCCCGTCCACGACTGTTGTCCTTACTGCCCAAGGAAGGGGA
TTCCGTCGAAGGGCAGGTGCTGACAACAGGAATGACGGGTTCCCTCCCT

910 920 930 940 950
GCATGAAACCCACCACTGGTCCTGCGACCCACTGTCTTTGGAATCCACCC
CGTACTTTGGGTGGTGACCAGGACGCTGGGTGACAGAAACCTTAGGTGGG

960 970 980 990 1000
CAGGAGCCCAGGAGCCTTGCCTGACACTTGGATTTACTTCTTTATCAAGC
GTCTCGGGTCTCGGAACGGACTGTGAACCTAAATGAAGAAATAGTTTCG

1010 1020 1030 1040 1050
ATCCATCTGACTAAGGCACAAATCCAACATGTTACTGTTACTGATACAGG
TAGGTAGACTGATTCCGTGTTTAGGTTGTACAATGACAATGACTATGTCC

1060 1070 1080 1090 1100
AAAAACAGTAACCTTAAGGAATGATCATGAATGCAAAGGGAAAGAGGAAAA
TTTTTGTCAATTGAATTCCTTACTAGTACTTACGTTTCCCTTTCTCCTTTT

1110 1120 1130 1140 1150
GAGCCTTCAGGGACAAATAGCTCGATTTTTTGTAAATCAGTTTCATACAA
CTCGGAAGTCCCTGTTTATCGAGCTAAAAAACATTTAGTCAAAGTATGTT

1160 1170 1180 1190 1200
CCTCCCTCCCCCATTTTCAATTCTTAAAAGTTAATTGAGAATCATCAGCCAC
GGAGGGAGGGGGTAAAGTAAGAATTTTCAATTAACCTTAGTAGTTCGGTG

1210
GTGTAGGGTGTGAG
CACATCCCACTC

Table 6. Localization of naturally occurring single nucleotide polymorphisms (SNPs) in human α_1 AR coding region

| Amino Acid Position | Amino Acid Change | SNP Name (dbSNP ID, handle, release date) | Nucleotide Position | Nucleotide Change | Domain Position | All | All (Except Coriell) | Black | Hispanic | Caucasian |
|---------------------|-------------------|---|---------------------|-------------------|-----------------|-------|----------------------|-------|----------|-----------|
| 5 | None | | 15 | G→C | N-terminus | 0.002 | 0.003 | 0.000 | 0.000 | 0.005 |
| 154 | Ser→Ala | S154A (G2286a1*) | 460 | T→G | TM4 | 0.007 | 0.005 | 0.000 | 0.013 | 0.005 |
| 166 | Arg→Lys | R166K | 497 | G→A | TM4 | 0.002 | 0.003 | 0.000 | 0.000 | 0.005 |
| 200 | Ile→Ser | I200S (rs2229125, WICVAR, 8/15/01) | 599 | T→G | TM5 | 0.005 | 0.005 | 0.000 | 0.000 | 0.010 |
| 247 | Gly→Arg | G247R (rs3730287, WIPGA, 8/28/02) | 739 | G→A | IL3 | 0.003 | 0.003 | 0.000 | 0.023 | 0.000 |
| 311 | Val→Ile | V311I | 931 | G→A | TM7 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 |
| 347 | Arg→Cys | R347C (rs1048101, TSC-CSHL, 1/29/01) | 1039 | C→T | C-terminus | 0.463 | 0.482 | 0.267 | 0.525 | 0.565 |
| 401 | None | | 1203 | T→G | C-terminus | 0.002 | 0.003 | 0.012 | 0.000 | 0.000 |
| 465 | Glu→Asp | E465D (rs2229126, WICVAR, 8/15/2001) | 1395 | A→T | C-terminus | 0.030 | 0.021 | 0.023 | 0.025 | 0.020 |

Nucleotide number is based on the first nucleotide of the start codon being +1 of human α_1 AR cDNA (GeneBank accession number is L31774).

TM: transmembrane region; IL: intracellular loop. SNPs are identified from 281 individuals: Coriell n=90 (enriched for minorities but exact race not known), Black n=43, Hispanic n=40, caucasian n=101. *It is a Whitehead Internal ID cited from website <http://www.cardiogenomics.org>.

TABLE 7. Agonist and Antagonist Binding Affinities of Human α_{1A} AR Wild Type and SNPs from High-expression Stable

| Clones | | α_{1A} AR WT | S154A | R166K | I200S | G247R | V311I | R347C | E465D |
|--|---|---------------------|-----------|-------------|-------------|-----------|-------------|------------|------------|
| Domain location | — | — | TM4 | TM4 | TM5 | IL3 | TM7 | C-terminus | C-terminus |
| Expression (pmol/mg) | | 1.77±0.24 | 1.53±0.07 | 2.37±0.28 | 1.53±0.10 | 1.96±0.40 | 1.75±0.37 | 1.76±0.22 | 2.02±0.27 |
| [¹²⁵ I]HEAT(K_d , pmol/L) | | 42.1±6.5 | 38.1±4.4 | 35.9±10.0 | 34.5±1.3 | 32.1±5.3 | 42.7±16.5 | 39.9±3.2 | 38.8±3.7 |
| Agonists (pK _i) | | | | | | | | | |
| Norepinephrine | | 4.73±0.03 | 4.73±0.08 | 4.34±0.10** | 4.90±0.08 | 4.61±0.03 | 4.34±0.06** | 4.73±0.03 | 4.64±0.02 |
| Epinephrine | | 5.01±0.02 | 4.87±0.06 | 4.64±0.04** | 5.18±0.08 | 4.96±0.01 | 4.57±0.08** | 5.01±0.05 | 4.91±0.04 |
| Phenylephrine | | 4.69±0.04 | 4.60±0.08 | 4.44±0.01* | 4.82±0.07 | 4.58±0.05 | 4.27±0.02** | 4.69±0.04 | 4.75±0.06 |
| Oxymetazoline | | 7.67±0.02 | 7.57±0.02 | 7.61±0.04 | 7.84±0.10 | 7.64±0.03 | 7.82±0.03 | 7.58±0.07 | 7.57±0.08 |
| Antagonists (pK _i) | | | | | | | | | |
| Prazosin | | 9.39±0.10 | 9.34±0.09 | 9.19±0.08 | 9.69±0.10 | 9.40±0.14 | 9.20±0.06 | 9.30±0.07 | 9.61±0.10 |
| Phentolamine | | 7.70±0.03 | 7.77±0.05 | 7.77±0.04 | 7.20±0.05** | 7.60±0.07 | 7.60±0.04 | 7.75±0.01 | 7.84±0.01 |
| 5-Methylurapidil | | 8.44±0.04 | 8.45±0.10 | 8.38±0.08 | 8.40±0.07 | 8.45±0.07 | 8.87±0.06** | 8.39±0.02 | 8.44±0.04 |

pK_i values for the binding of agonists and antagonists were determined in competition binding experiments on rat-1 cell membranes stably transfected to express α_{1A} AR WT or its SNPs (receptor density > 1.5 pmol/mg protein). K_d values for the antagonist [¹²⁵I]HEAT and receptor densities were determined from saturation binding studies. * P <0.05, ** P <0.01 compared with α_{1A} AR WT. Data are reported as the mean±SEM of 3-7 different experiments.

TABLE 8. Agonist and Antagonist Binding Affinities of Human α_{1A} AR Wild Type and SNPs from Low-expression Stable

| Clones | | α_{1A} AR WT | S154A | R166K | I200S | G247R | V311I | R347C | E465D |
|--|-----------|---------------------|-------------|-------------|-----------|-------------|-----------|------------|------------|
| Domain location | — | — | TM4 | TM4 | TM5 | IL3 | TM7 | C-terminus | C-terminus |
| Expression (pmol/mg) | 0.36±0.01 | 0.37±0.09 | 0.44±0.05 | 0.21±0.06 | 0.33±0.03 | 0.29±0.03 | 0.36±0.01 | 0.26±0.05 | |
| [¹²⁵ I]HEAT(K_d , pmol/L) | 42.9±4.0 | 37.7±16.3 | 42.6±6.1 | 49.9±7.7 | 49.1±10.8 | 49.7±10.0 | 50.7±9.8 | 46.6±16.4 | |
| Agonists (pK_i) | | | | | | | | | |
| Norepinephrine | 4.73±0.08 | 4.78±0.02 | 4.31±0.04** | 4.82±0.07 | 4.77±0.09 | 4.32±0.04** | 4.65±0.04 | 4.65±0.04 | |
| Epinephrine | 5.02±0.07 | 4.97±0.02 | 4.62±0.03** | 5.15±0.03 | 5.09±0.13 | 4.36±0.01** | 4.97±0.08 | 4.90±0.10 | |
| Phenylephrine | 4.68±0.08 | 4.72±0.07 | 4.37±0.04** | 4.75±0.03 | 4.60±0.08 | 4.24±0.03** | 4.62±0.03 | 4.66±0.11 | |
| Oxymetazoline | 7.65±0.02 | 7.78±0.03 | 7.63±0.06 | 7.65±0.01 | 7.56±0.04 | 7.78±0.02 | 7.75±0.02 | 7.76±0.09 | |
| Antagonists (pK_i) | | | | | | | | | |
| Prazosin | 9.51±0.11 | 9.36±0.09 | 9.32±0.08 | 9.54±0.04 | 9.40±0.14 | 9.50±0.03 | 9.47±0.12 | 9.22±0.11 | |
| Phentolamine | 7.68±0.03 | 7.64±0.01 | 7.73±0.04 | 7.31±0.07** | 7.60±0.07 | 7.49±0.10 | 7.70±0.05 | 7.76±0.11 | |
| 5-Methylurapidil | 8.42±0.11 | 8.38±0.07 | 8.41±0.15 | 8.43±0.07 | 8.45±0.07 | 8.94±0.06** | 8.56±0.04 | 8.48±0.04 | |

pK_i values for the binding of agonists and antagonists were determined in competition binding experiments on rat-1 cell membranes stably transfected to express α_{1A} AR WT or its SNPs (receptor density < 0.5 pmol/mg protein). K_d values for the antagonist [¹²⁵I]HEAT and receptor densities were determined from saturation binding studies. ** P <0.01 compared with α_{1A} AR WT. Data are reported as the mean±SEM of 3-5 different experiments.

Table 9 Functional alterations and clinical implications of human α_1 -AR SNPs

| SNP | Functional Alteration(s) | Possible Biological Mechanisms | Clinical Implications |
|-------|--|---|--|
| R166K | Decreases binding affinity for endogenous agonists, modestly reduces potency of NE in stimulating IP_3 formation | Hampers agonist binding to residue F163 | 1) The homozygous form might provide a novel mechanism underlying human hypotension syndromes, 2) may protect against sympathetically-mediated hypertension |
| I200S | Decreases binding affinity for antagonist phentolamine | Influences three consecutive residues (Q177, I178, N179) involved in phentolamine binding | May explain variable individual response to drug treatments |
| G247E | Enhances receptor activity and stimulates cell growth | Unknown | 1) Might be relevant to cardiovascular remodeling (e.g. in hypertension, atherosclerosis, myocardial hypertrophy) and benign prostatic hyperplasia, 2) May be important in neoplastic transformation (e.g. some cancers such as prostate cancer) |
| V311I | Decreases binding affinity for endogenous agonists, reduces potency of NE in stimulating IP_3 formation | Stabilizes the salt-bridge | Same as SNP R166K |